

13	364	1	US-08-036-623A-5	Sequence 5, APP11
14	361.5	1	US-08-331-004A-1	Sequence 1, APP11
15	361.5	1	US-08-331-004A-1	Sequence 1, APP11
16	350.5	1	US-08-908-758-1	Sequence 1, APP11
17	339.5	1	US-07-763-705A-13	Sequence 13, APP11
18	338.5	1	US-07-783-705A-11	Sequence 11, APP11
19	326	4	US-08-980-832-1	Sequence 1, APP11
20	326	4	US-08-832-27	Sequence 27, APP11
21	324	3	US-08-660-645A-4	Sequence 4, APP11
22	324	3	US-09-298-718-4	Sequence 4, APP11
23	324	4	US-09-516-969-4	Sequence 4, APP11
24	176.5	7.8	US-08-096-623A-16	Sequence 16, APP11
25	176.5	7.8	US-08-036-623A-17	Sequence 17, APP11
26	174	7.7	US-09-091-725-18	Sequence 18, APP11
27	174	7.7	US-09-091-725-12	Sequence 12, APP11
28	170	7.5	US-09-060-756-345	Sequence 345, APP11
29	159	4.0	US-09-051-725-22	Sequence 22, APP11
30	136.5	6.0	US-08-351-981-1	Sequence 1, APP11
31	121	5.3	US-08-331-981-5	Sequence 5, APP11
32	116	5.3	US-09-625-188-3	Sequence 3, APP11
33	116	5.1	US-08-310-693-1	Sequence 1, APP11
34	116	5.1	PCT-US95-11280-1	Sequence 1, APP11
35	112.5	5.0	US-08-260-546-10	Sequence 10, APP11
36	112.5	5.0	US-09-446-604-12	Sequence 12, APP11
37	111.5	4.9	US-09-060-756-42	Sequence 427, APP11
38	107.5	4.7	US-09-060-756-545	Sequence 545, APP11
39	104.5	4.6	US-08-351-981-3	Sequence 3, APP11
40	101	4.4	US-08-357-653-175	Sequence 175, APP11
41	101	4.4	US-08-833-516-8	Sequence 78, APP11
42	101	4.4	US-08-759-038-114	Sequence 114, APP11
43	101	4.4	US-08-758-314-114	Sequence 114, APP11
44	100.5	4.3	US-08-642-233A-1	Sequence 1, APP11
45	97	4.3	US-07-602-733C-3	Sequence 3, APP11
46	43	4.3	49377	
47	43	4.3	20235	

ALIGNMENTS

RESULT 1

US-08-579-667-5

; Sequence 5, Application US/08579667

; Patent No. 5705624

; GENERAL INFORMATION:

; APPLICANT: Fitzmaurice, Wayne P.

; APPLICANT: Hellmann, Gary M.

; APPLICANT: Grill, Laurence K.

; APPLICANT: Kumagai, Motoo H.

; APPLICANT: Della-Cioppa, Guy R.

; TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN

; TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Virginia C. Bennett

; STREET: 1211 East Morehead Street, PO Drawer 34009

; CITY: Charlotte

; STATE: No. 5705624th Carolina

; COUNTRY: USA

; ZIP: 28234

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/579,667

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Bennett, Virginia C.

; REGISTRATION NUMBER: 37,092

; REFERENCE/DOCKET NUMBER: 627-196

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-420-2200

; FAX: 919-481-3175

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Command line parameters:
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-QFEXT=0 -UnitsBits -START=1 -END=1 -MATRIX=blocum62 -TRANS=human40 cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFILE=pco -NOM=ext -HEAPSIZ=500 -MINLEN=2000000000
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-YGAPOP=10 -TGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Prep. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	DB			
1	1826	80.4	1826	1	US-08-579-667-5		Sequence 5, AppI11
2	1799	79.3	1814	1	US-08-579-667-7		Sequence 7, AppI11
3	1774	78.1	1795	1	US-08-579-667-7		Sequence 1, AppI11
4	1762	77.6	1316	1	US-08-579-667-3		Sequence 3, AppI11
5	1750	77.1	1239	4	US-09-180-342-2		Sequence 2, AppI11
6	1744	76.8	1239	4	US-09-180-342-2		Sequence 1, AppI11
7	1732	76.3	1646	1	US-07-995-950-2		Sequence 2, AppI11
8	1732	76.3	1646	1	US-08-300-512-2		Sequence 2, AppI11
9	442	19.5	749	1	US-08-779-667-9		Sequence 9, AppI11
10	364	16.0	1198	1	US-08-095-726-5		Sequence 5, AppI11
11	364	16.0	1198	1	US-08-096-043-5		Sequence 5, AppI11
12	364	16.0	1198	1	US-08-093-577-5		Sequence 5, AppI11


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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE: NAME/KEY: CDS
; LOCATION: 362..1591
; US-08-579-667-1

Alignment Scores:
Score: 1.96e-198
Percent Similarity: 174.00
Best Local Similarity: 87.07%
Query Match: 79.59%
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Db: 1 MetSerMetSerValAlaLeuLeu
Db: 356 CTCAGATGTCGTGCTGTGCTGTGTA
Qy 21 ThrGlyLeuLeuAspSerValArg
Db: 413 ACAGGATTCTCTGGATCAATTGGG
Qy 41 AlaArgAspArgAsnLeuMetTrp
Db: 470 -----AGAAATTAGTGTGCC
Qy 61 AsnPheGlySerLeuIleAlaAsp
Db: 521 ATTGGT-----.
Qy 81 LysGlySerThrPheSerValGln
Db: 530 -----TCGTAAAGGG
Qy 100 ThrValSerSerGluIleLysVal
Db: 575 ACATGACATCGAACAGATGGTT
Qy 120 ArgGlnIleArgSerThrAspAsp
Db: 635 AGGAGTTGAGACTACTGATGATG
Qy 140 LeuGlyLeuLeuSerGluAlaTyr
Db: 695 TTGAGCTGGTGTGAGTGAAGCATAT
Qy 160 ThrPhenylLeuGlyIleIleLeu
Db: 755 ACATTTTACTAGGAACCATGCTA
Qy 180 TyrValTrpCysArgArgThrAsp
Db: 815 TATGATGGTGCAGGAGACAGAT
Qy 200 ProGlnAlaLeuAspArgTrpGlu
Db: 875 CCACAGCTTGAATAGTGTGGAA
Qy 220 AspMetIleAspAlaAlaLeuSer
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Qy 240 PheArgAspMetIleGluGlyMet
Db: 995 TTGAGATATGATGAGGAATGAGGAATG

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QY 260 ASPGlutLeutTrLeutTrCystTrTrValAlaGlyThrValcLeuMetSerValPro 279
 QY 1055 GATGACTATACCTATTTGTTAGTGTGCGGGTGTAGCTGTTCA 1114

QY 280 ValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTrAsnAlaAlaLeu 299
 Db 1115 ATTATGGTATGCACTGATCAAGGCAACAGAGAACTATAATGCGCTTGG 1174

QY 300 AlaLeuGlyIleLeuAlaLysGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArg 319
 Db 1175 GCTTGGTATGCAATCAACAACTACTCGAGAACTGAGATGCGAGAAATGCGCAGA 1234

QY 320 ArgGlyArgValTrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAsp 339
 Db 1235 AGGGAGAGGAGCTACTACCTCAAGATGAATTAGCACATGCAAGTGTCTCGAGGTGAC 1294

QY 340 IlePheAlaGlyArgValThrAspLysTrpArgAsnPheMetLysGlnIleGlnArg 359
 Db 1295 ATATTGCTGAAAAGTGACGCTTAATGGAGAAAGCTTATGAAAGCAAAATCGAGGG 1354

QY 360 AlaArgLysPheAspGluSerGlyIleGlyValThrGluLeuAspSerAlaSerArg 379
 Db 1355 GCAAGAAAGTCTCTTGATGAGGAGTGCACAACTGAGCTCAGCTAGCTAGATA 1414

QY 380 TrpProValLeuThrAlaLeuLeuLeuLeuArgLysIleLeuAspGluIleGluAlaAsn 399
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QY 420 ProIleAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
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QY 439 S 439
 Db 1595 G 1595

RESULT 4
 US-08-179-667-3
 ; Sequence 3 , Application US/08379667
 ; Patent No. 5704624
 GENERAL INFORMATION:
 / APPLICANT: Fitzmaurice, Wayne P.
 / APPLICANT: Heilmann, Gary M.
 / APPLICANT: Grill, Laurence K.
 / APPLICANT: Kumagai, Monto H.
 / APPLICANT: Della-Cioppa, Guy R.
 TITLE OF INVENTION: DNA SEQUENCES ENCODING ENZYMES USEFUL IN
 TITLE OF INVENTION: PHYTOENE BIOSYNTHESIS
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Virginia C. Bennett
 STREET: 1211 East Morehead Street, PO Drawer 34009
 CITY: Charlotte
 STATE: No. 5705624th Carolina
 COUNTRY: USA
 ZIP: 28234

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION NUMBER: US/08/579,667
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Virginia C.
 REGISTRATION NUMBER: 37,092

REFERENCE/DOCKET NUMBER: 627-196
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-420-2200
 TELEFAX: 919-881-3175
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1316 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1239
 -08-579-667-3

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 aligned. No.: 1 1762.00
 score: 87.04%
 Percent Similarity: 80.32%
 Local Similarity: 77.62%
 Query Match: 1
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 23 LeuLeuAspSerValArgGlnGlyAsnArgV
 58 TTCTGGATTCAATCCGGAGGAAACCGGG
 43 AspArgAsnLeuMetTrpAspGlyArgL
 106 CATAGGATTGTGTCGCAAGGAGAACAA
 63 GlySerLeuIleAlaAspProArgTyrSerC
 166 GGT-----
 83 SerThrPheSerValGlnSerSerLeuValA
 169 -----TCGTTAAAGTCGCTATGGTGG
 102 SerSerGluLysValTrpAspValValI
 220 ACATCAGACATGGTTAGATGTTGGTGTAT
 122 LeuArgSerThrAspSerPheGluValLysP
 280 TTGAGATCTAGTGTGATTAGATGAACTGAAG
 142 LeuLeuSerGluLataTrpArgCysGlyG
 340 TCTGGTGTGAGCATATGATAGGGTGTAGGG
 162 TyrLeuGlyThrLysLeuMetThrProGluA
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 182 TrpCysArgGlnThrAspGluLeuValAsP
 460 TGTTGAGGAAACAGACGAACTGTGTGANG
 222 LeuAspAlaAlaLeuSerAspThrValSerA
 202 AlaLeuAspSerTrpGluThrArgLeuGluA
 520 GCCTTAGTAGTGTGGAAAGACGGCTGGANG
 580 CTCGATGTCGCTTGTGTCGAAGACTGTTCCAA

APPLICANT: Mukharrli, Indrani
 APPLICANT: Proffitt, John H.
 APPLICANT: Yarger, James G.
 APPLICANT: Yen, Huei-Che B.
 TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
 Glycosylated Zeaxanthin In Genetically Engineered Host
 NUMBER OF SEQUENCES: 104
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Welsh & Katz, Ltd.
 STREET: 120 S. Riverside Plaza, 22nd Floor
 CITY: Chicago
 STATE: IL
 COUNTY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08-096,623A
 FILING DATE: 22-JUL-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/805,061
 FILING DATE: 09-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/662,921
 FILING DATE: 28-FEB-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/562,674
 FILING DATE: 03-AUG-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/525,551
 FILING DATE: 18-MAY-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/487,613
 FILING DATE: 02-MAR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Gamson, Edward P.
 REGISTRATION NUMBER: 29,381
 REFERENCE/DOCKET NUMBER: AMO-006.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 655-1500
 TELEFAX: (312) 655-1501
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1198 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 POSITION IN GENOME:
 MAP POSITION: -15 to 1183
 UNITS: bp
 US-08-096,623A-5
 Alignment Scores:
 Pred. No.: 4.65e-33 Length: 1198
 Score: 364.00 Matches: 95
 Percent Similarity: 50.53% Conservative: 49
 Best Local Similarity: 33.33% Mismatches: 124
 Query Match: 16.04% Indels: 18
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 QY 168 MetThrProGluArgArgGluGlyGluValCysAlaLysThrPheTyLeuGlyThrLysLeu 187

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Qy	188	GlutLeuValAspGlyProAsn ---	-AlaserHisslerhr 199
Qy	157	GACGTCTATTGACGCCAGACCCACGGCTTCGCAAGGAGGCCGGAGGGAGGCC	216
Db	200	ProGlnAlaLeuAspArgTrpLeuThrArgLeuGluAspSerLeuPheSerGlyArgProPhe	219
Db	217	ACCCAGGGCTCGCCCGCTGGCACCCCTGACCCCTGAGGGCCGAGATGAGGGCCGAGATG	276
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Qy	1		
Db	277	CGGGATCGGGCTTCGTCGCTTCAGAGGTGGCTGACCCACAGGTATTACGGCCCG	336
Qy	239	ProPheArgAspMetIleGluGlyMetArgMetAspLeuTrpLeuSerArgTrpLysThr	258
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Qy	259	PhAspGluLeuTrpLeuTrpCystTrpTrpValAlaGlyThrValGlyLeuMetSerVal	278
Db	397	TTCGAGGATAACGCTGCGCTACTGCTTCACGTGGCGGCGTGGGTCTATGAGGGCC	456
Qy	279	ProValMetGlyIleAlaProGluSerLeuLysAlaThrThrGluSerValTyrosAlaAla	298
Qy	1		
Db	457	AGGGATGGGGGGG-----CGGATGAGGGGGTGTGATGGCC	498
Qy	299	LeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAla	318
Db	499	TGGGATCTGGGCTGGCTGGCTTCAGCTGACGAATATGCCCGGATATTATGACATGTCG	558
Qy	319	ArgArgGlyArgValTrpLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGlu	338
Db	559	GCTATTGACCGCTGGCATCTGCCCCGCGAGTGGCTCAGGATGCGGGCTGGCCGGAG	618
Qy	339	AspIlePheAla-GlyArgValThrAspLysTrpArgAsnPheMetLysGlnIleGln	358
Qy	1		
Db	619	AACTATGCCGCCGGAAATGCCCCGGCTGGG-TGG--CGGAGCTTATGTA	674
Qy	358	DArgAlaArgGlySpHeAspGluSerGluLysGlyValTrpGluLeuAspSerAlaLe	378
Db	675	TCCGCAGAGCGCTACTACATCTCCACGCCGCTCACGATCTGGCGGGCCT	734
Qy	378	rArgTrpProValLeuThrAlaLeuLeuLeuArgLysIleLeuAspGluIleGluGluAla	398
Db	735	CCCGTGGCGATGCCGCCGCCACGCCGAGCTACGGCTATTAGGTTAAAGGC	794
Qy	398	AsnAsnAspTrpAsnAsnPheThrArgGlnAlaArgGlnAlaArgLysProLysLeuLeuLeu	418
Qy	1		
Db	795	GCGGGGGCGGGCTGGATGCCACACAGAAAGTGAAATAATGCCAT	854
Qy	418	rLeuProIleAla 422	
Db	855	GCTGATGGGGCA 867	
RESULT	14		
US-0-0-331-004A-1			
;	Sequence 1, Application US/08331004A		
;	Patent No. 5618988		
;	GENERAL INFORMATION:		
;	APPLICANT: Hauptmann, Randal		
;	APPLICANT: Eschenfeldt, William H		
;	APPLICANT: Brinkhaus, Friedhelm L		
;	TITLE OF INVENTION: Enhanced Carotenoid Accumulation		
;	TITLE OF INVENTION: In Storage Organs of Genetically		
;	TITLE OF INVENTION: Engineered Plants		
;	NUMBER OF SEQUENCES: 9		
;	CORRESPONDENCE ADDRESS:		
;	ADDRESSEE: Amoco Corporation, Law Dept		
;	STREET: 55 Shuman Boulevard, Suite 600		
;	CITY: Naperville		
;	STATE: IL		
;	COUNTRY: USA		

339 AspIlePheAla-GlyArgValThrAspLysIlePheMetLysGlnIleG1 358
 QY ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 606 RACTGCGCGGAGATTCGGCCGGTGGCTGGCGCTGGG-GAGGGCTATTGA 664
 358 nAqGalaArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSe 378
 DDB ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 665 TGCCTGAGGCCGTACTACATCTCCAGGGGTACACCAATCTCCGGCGCTG 724
 QY ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 378 rArgPheProValLeuIleAlaLeuLeuIleArgLysIleLeuAspCysIleGluAl 398
 DDB ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 725 CGCGGGATCCACGGCCAGCTACGGGATCTACGGGATCTGGGATTAAGGTAAGGC 784
 QY ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 398 aAsnAspTyrAsnAsnPheThrArgArgAlaTyrValSerLysProLysLeuLeuIth 418
 DDB ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 785 GGCGGAGCCGCGCCCTGGATCCGGCAGCACCCAGCAAACTGAAAAATTGCCAT 844
 418 rLeuProLeaAla 422
 QY ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 DDB ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
 845 GCTGATGCGGGCA 857

RESULT 15
 PCT-US95-13937A-1
 Sequence 1, Application PC/TUS9513937A
 GENERAL INFORMATION:
 APPLICANT: Hauptmann, Randal
 APPLICANT: Eschenfeldt, William H
 APPLICANT: English, Jami
 APPLICANT: Brinkhaus, Friedhelm L
 TITLE OF INVENTION: Enhanced Carotenoid Accumulation
 TITLE OF INVENTION: In Storage Organs of Genetically
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amoco Corporation, Law Dept.
 STREET: 55 Shuman Boulevard, Suite 600
 CITY: Naperville
 STATE: IL
 COUNTRY: USA
 ZIP: 60563-8437
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/13937A
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Galloway, Norval B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 7087172447
 TELEFAX: 7087172430
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1083 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT/US95-13937A-1

Alignment Scores:
 Pred. No.: 7.77e-33 Length: 1083
 Score: 361.50 Matches: 95
 Percent Similarity: 50.18% Conservative: 48
 Best Local Similarity: 33.33% Mismatches: 126
 Query Match: 15.93% Indels: 17
 DB: 5 Gaps: 3

US-09-847-081B-2 (1-440) x PCT-US95-13937A-1 (1-1083)

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Db	24	GACCAAGCCACGGCAACCATGGCCACGGCAACAGTCGAAGAAGTTGCCCCACGGAGCTG	83
QY	168	MetThrProGluArgArgGalaIleTrrPalaIleTrrValTrrPcysArgArgThrAsp	187
Db	84	TTGCAACCCGGCCACCCGGCTAGGGCTGATGCCCTACACCTGGCCACGGAGCTG	143
QY	188	GluLeuvalAspGlyProAsn-----AlaserHistileThr	199
Db	144	GACCTCATGACGACAGACCAAGCCACGGCTTGGCACACGAGGCCGGAGGAGGCC	203
QY	200	ProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSerGlyArgProPro	219
Db	204	ACCCAGGCCCTGGCCCTGGCCGCTGCGCCTGCGCTGACCCCTGGCCGAGATG	263
QY	220	---AspMetLeuAspAlaLeuSerAspThrValSerArgPheProValAspIleGln	238
Db	264	CAGGATCCGGCTTGGCTGCGCTTTCAGGGTGGCTGCCACGGTTACGCCCGC	323
QY	239	ProPheArgAspMetIleGluGlyMetArgMetAspIleIutPlySerArgTyrlYsThr	258
Db	324	ATGGGCTTGATCACCTGACGGCTTGGATGGCTGAGTGGCTCAAGACCCGCTATGTCACC	383
QY	259	PhenylPheGluLeuTyrlLeuTyrlCysteTyrlValAlaGlyIthryvalGlyIleMetSerVal	278
Db	384	TTCAGGATACGCGCTACTGCTATCACGTGGGGCTGGTGGCTCATGATGGCC	443
QY	279	ProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValtyrasAlaAlaAla	298
Db	444	AGGGTGTATGGGCTG-----CGGATAGGGTGTGCTGGATCCGCC	485
QY	299	LeuAlaLenglyLeuAlaAsnGlnIleThrAsnIleLeuArgAspValGlyGluAspAla	318
Db	486	TGGCATCTGGCTGGCTTCCAGGTGACCAAATGCGCCGGATAATTATGACGATGCG	545
QY	319	ArgArgGlyArgValTyrlEuglyIleProGlnAspGluIleAlaIglnAlaGlyIleSerAspGlu	338
Db	546	GCTATGCGCTGCTATCTGCCCTCCGACTGGCTGAGGTGCGCTGACGGGAG	605
QY	339	AspIlePheAla-L-GlyArgValIthAspIlePheAspArgAsnPhemetylLysGlnIleG	358
Db	606	AACATGCGCCGGGGAGAATCGGCCGCCCTGGCCGGTGGCG-GAGGGCTTATTGAA	664
QY	358	nArgAlaArgLysPheAspGluUserGluLysIlyvalThrGluLeuAspSerAlaSe	378
Db	665	TGCCCAAGGCCGCTACTACATCTCCAGGGCTAACGATCTGCCGCCGCTACGATCTGCCGCCGCT	724
QY	378	rArgTrpProValLeuThrAlaLeuLeuLeuIutTyrlArgLysIleLeuAspGluIleGluIal	398
Db	725	CGCCGGGGATGCCGACGCCGCCGGAGCTACCGGAGATCGGTATTAAAGTAAAGC	784
QY	398	aaAsnAspTyrrAsnAsnPhenThrArgArgAlaItyValSerLysProLysLeuIleLeu	418
Db	785	GGGGAGGGCAGGCCGCTGGATGCCGCCAGCACCCAGCAAGGTAAGGAAATTGCCCCAT	844
QY	418	rLeuProIleAla-----	422
Db	845	GCTGTGGGCCA	857